

FIGURE 1

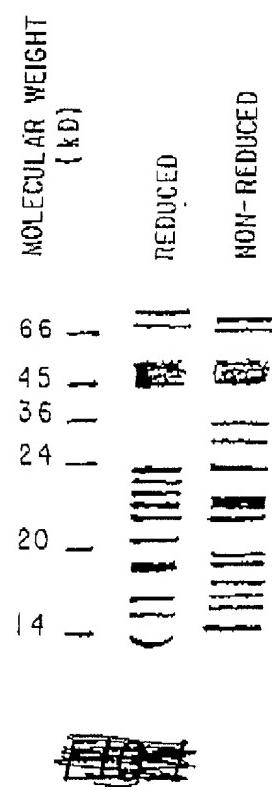


FIGURE ■ 2.

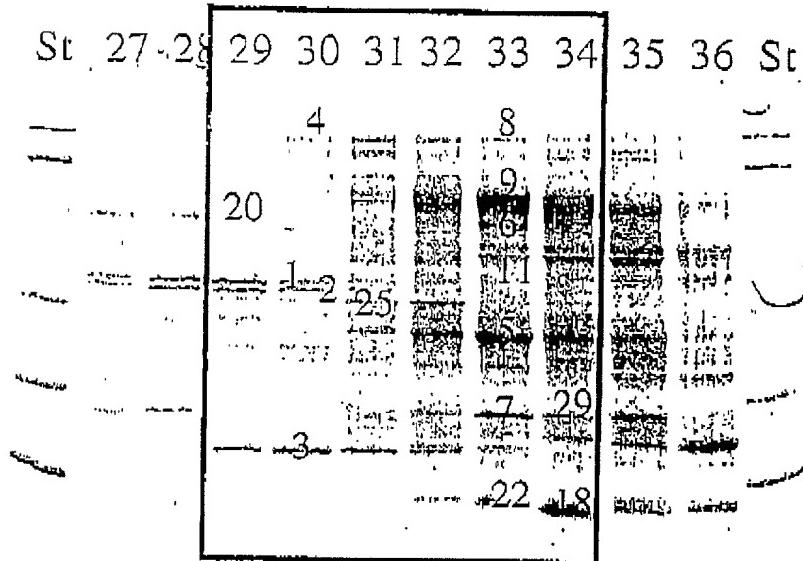
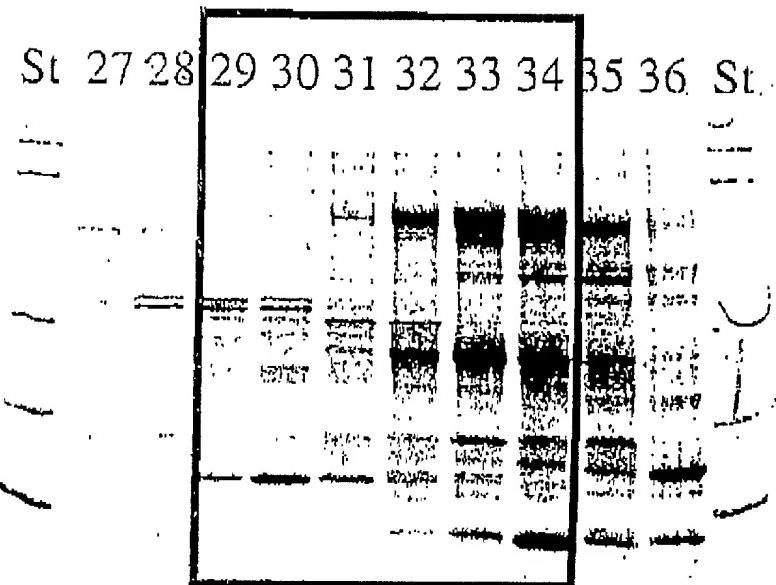
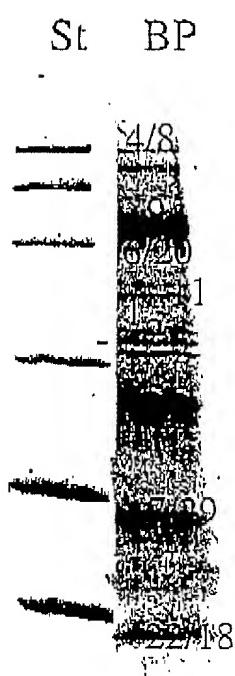


FIGURE ■ 3



Band No.	Identity
1	histone H1.c
2	histone H1.c
3	ribosomal protein RS20
4	similar to ribosomal protein LORP
5	BMP-3
6	$\alpha 2$ macroglobulin RAP & BMP-3
7	similar to ribosomal protein LORP
8	BMP-3
9	BMP-3
11	ribosomal protein RL6 & BMP-3
18	TGF- $\beta$ 2/SPP24
20	Factor H
22	TGF- $\beta$ 2
25	BMP-3 & H1.x
29	BMP-3 & ribosomal protein RL32

FIGURE 4

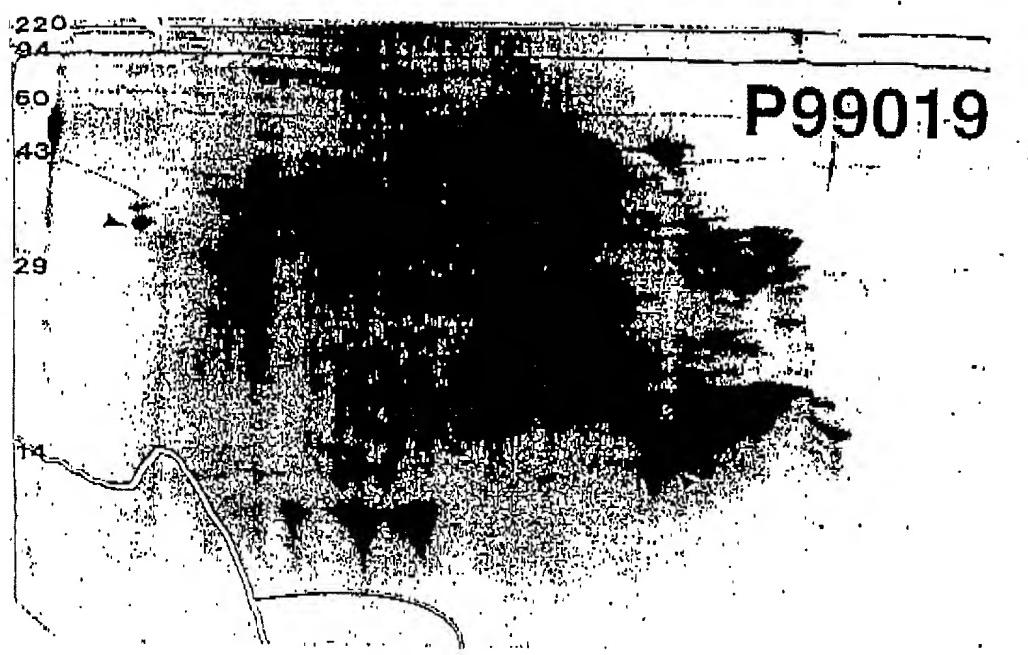
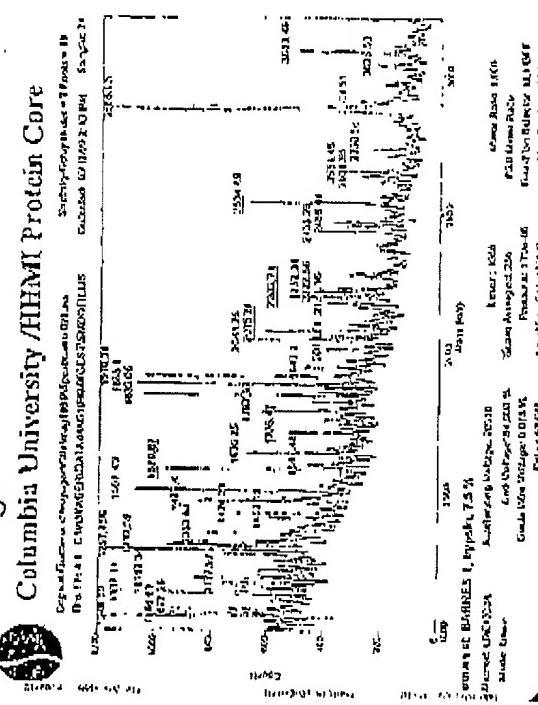
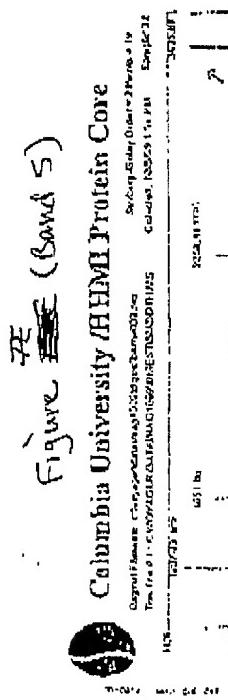


FIGURE 5



**Figure 7A. (Band 1)**

**Figure 7F (Band 6)**

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Figure 7G (Band 7)**

**Figure 7H (Band 8)**

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

**Columbia University IHMII Protein Core**

Digital Fingerprinter Version 2.000.19  
FingerPrint™ Electrophoresis System  
Sample ID: 114.P16 Sample 33

Wavenumbers: 3000, 2800, 1600, 1400, 1200, 1000 cm⁻¹.

Peaks labeled: 3021.45, 2913.07, 1733.53, 1654.12, 1613.62, 1513.29, 1413.29, 1302.24, 1202.24, 1102.24, 1002.24, 902.24, 802.24, 702.24, 602.24, 502.24, 402.24, 302.24, 202.24, 102.24, 100.3, 90.3, 80.3, 70.3, 60.3, 50.3, 40.3, 30.3, 20.3, 10.3, 10.0, 9.0, 8.0, 7.0, 6.0, 5.0, 4.0, 3.0, 2.0, 1.0, 0.0.

P. 04/06

FAX NO. 3039643101

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**Figure 7I** (Panel a)  
 Columbia University (UHM) Protein Concentration  
 Searched Database: UniProtKB/Swiss-Prot  
 Last Update: 2020-06-01  
 Total entries: 200000

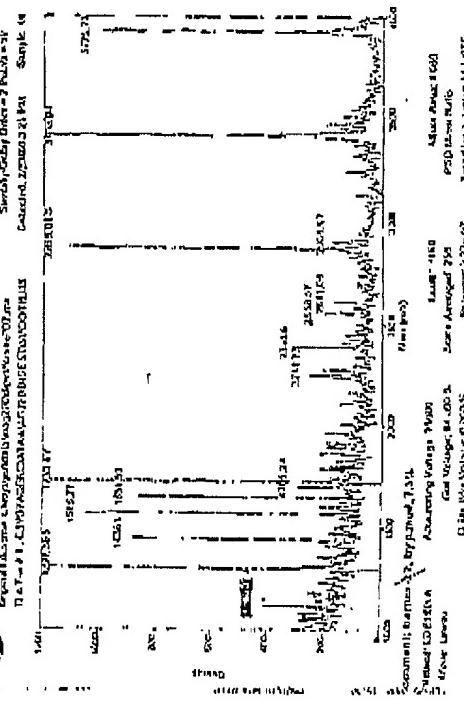
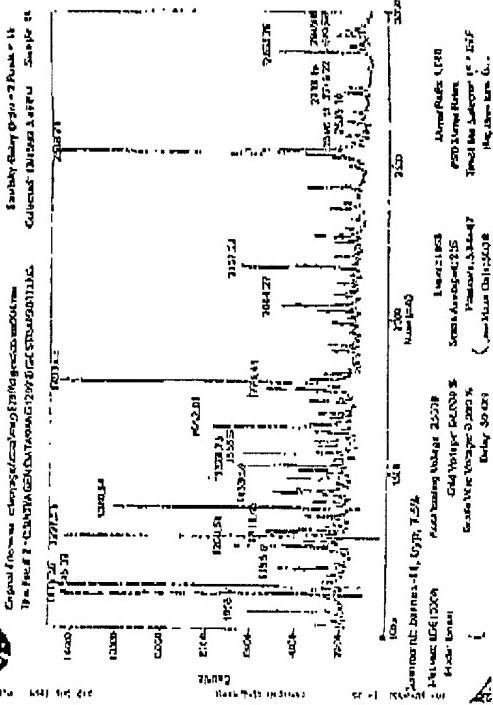


Figure 7J (Band 11)  
University MHEM Protein Core



Columbia University RHMI Protein Core

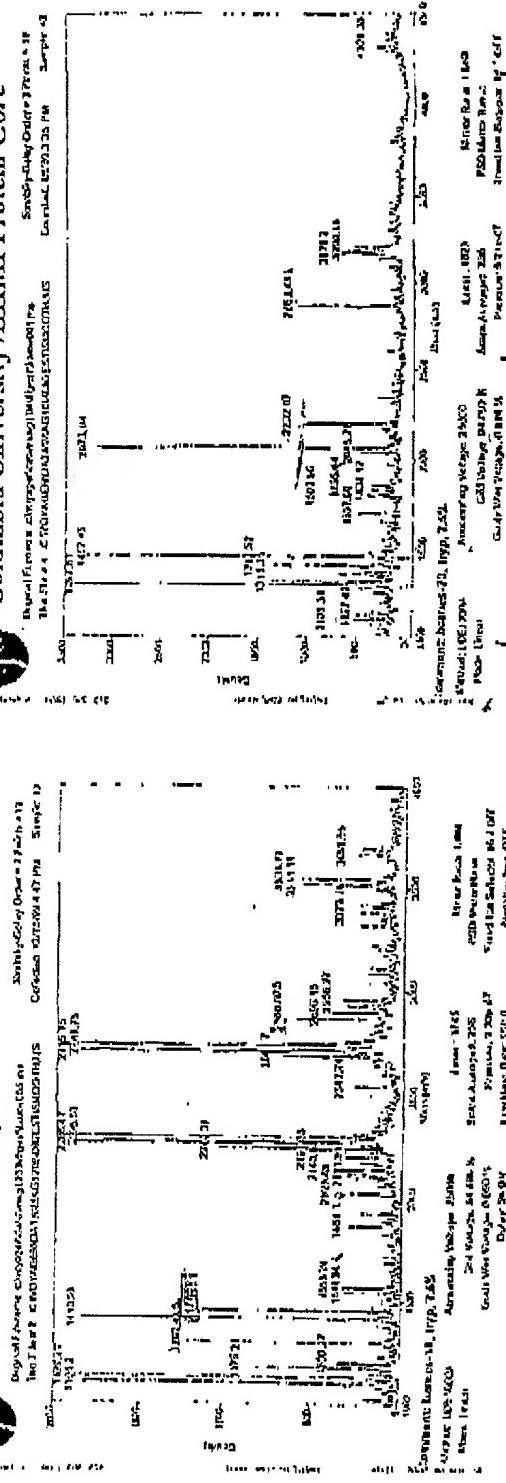
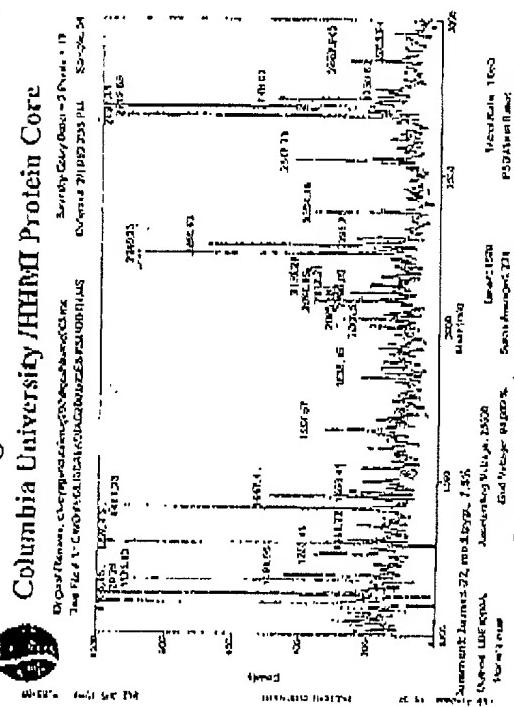


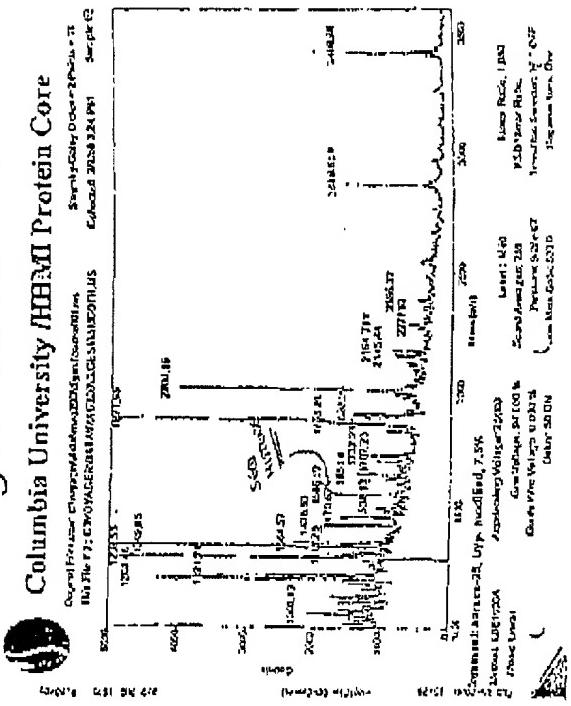
Figure 2 (Panel B)

## Figure 2E (Band 2D)

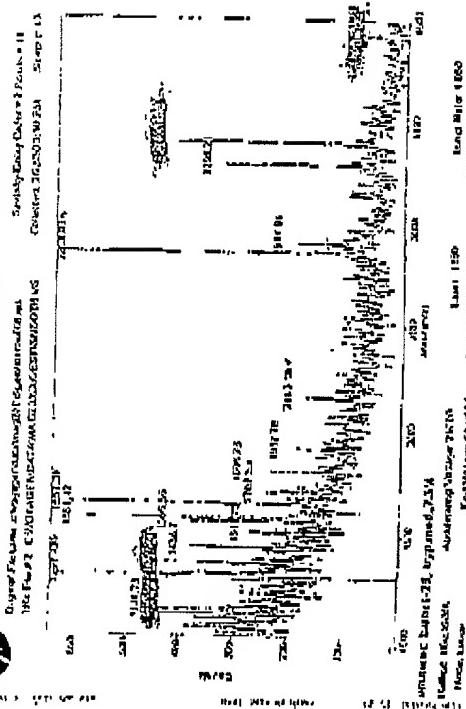
Figure ~~21~~ (Band 22)



Fugue in G major 25



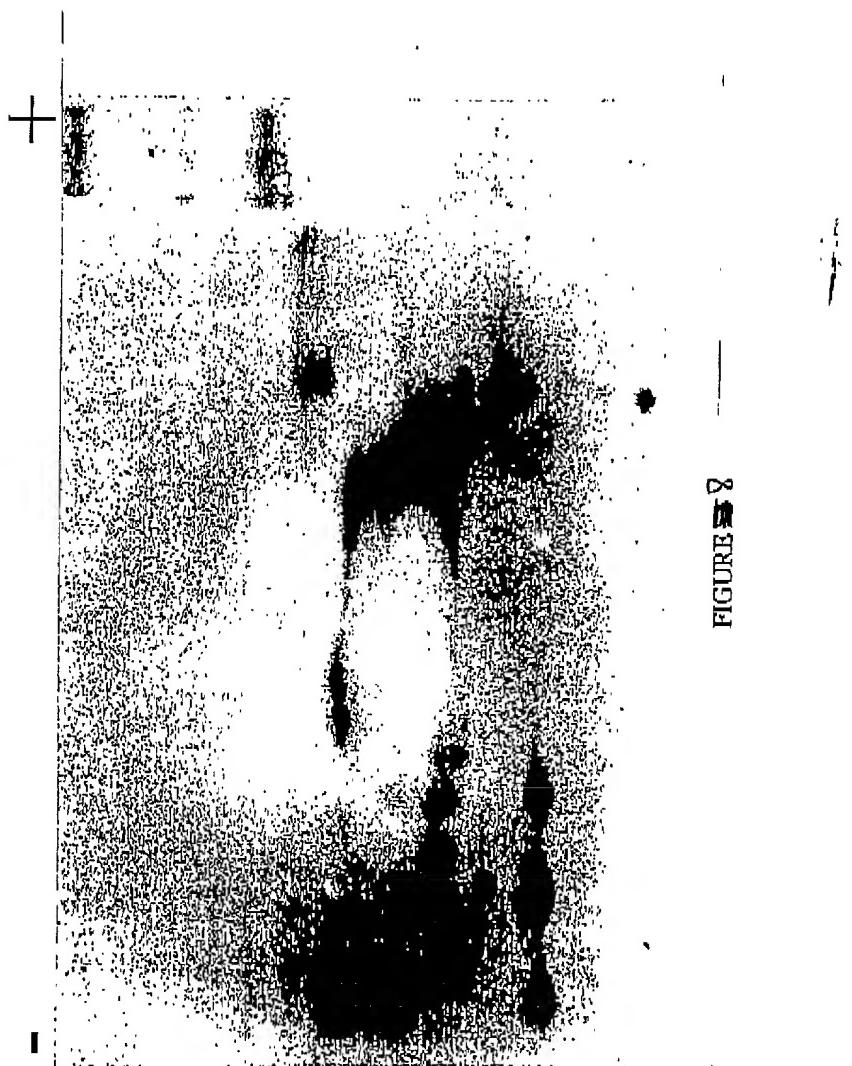
Columbia University /HHMI Protein Core



**Figure 70** (Band 29)

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FIGURE 9A

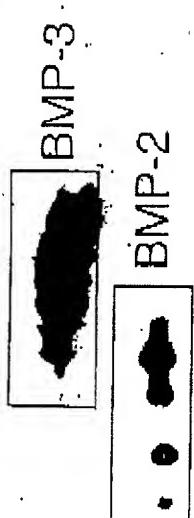


FIGURE 9B

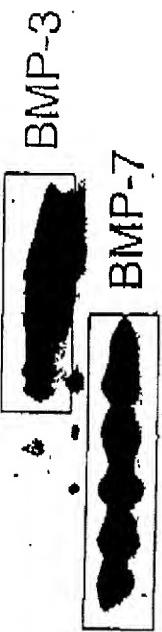


FIGURE 9C

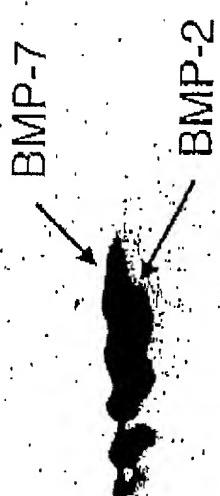


FIGURE 9D

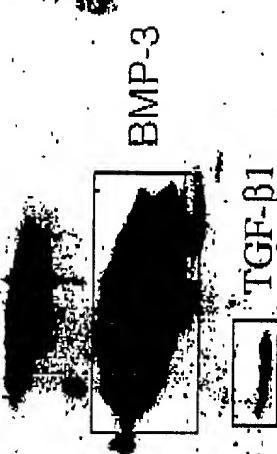


FIGURE 9B

52

FIGURE 10

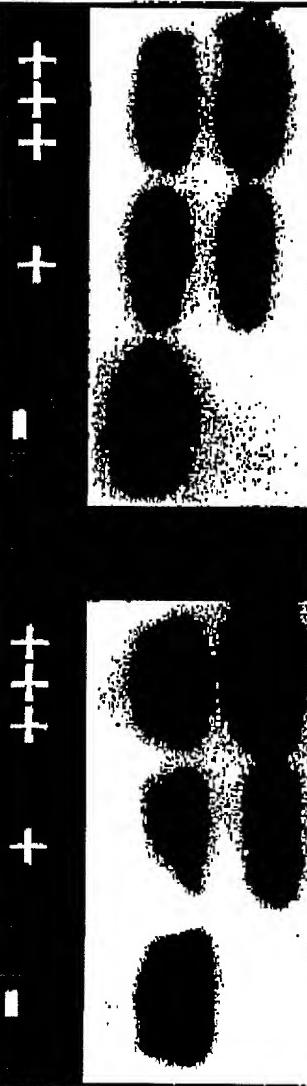
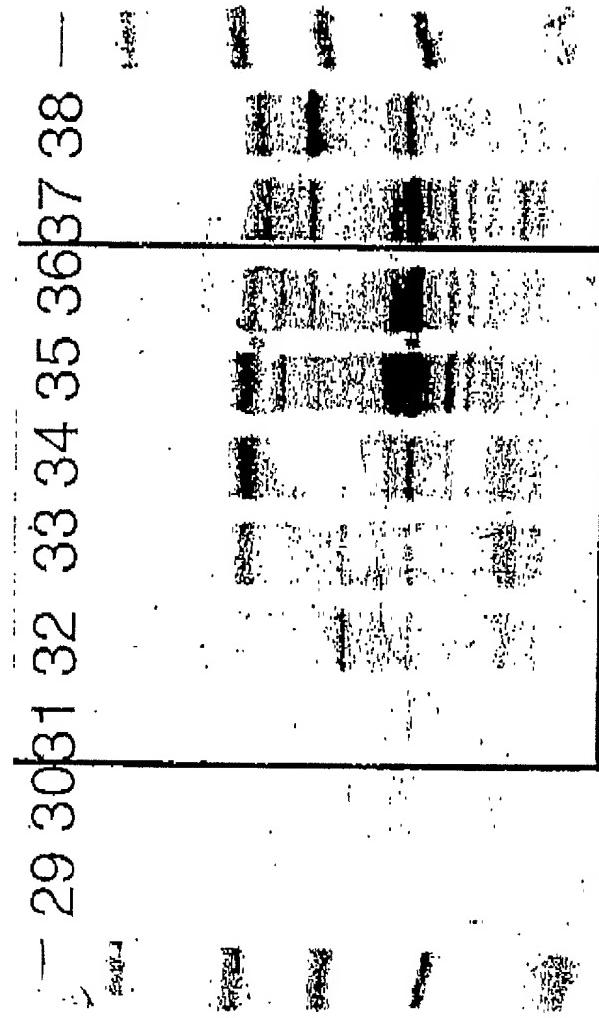


FIGURE 11

FIGURE 12

FIGURE 13A

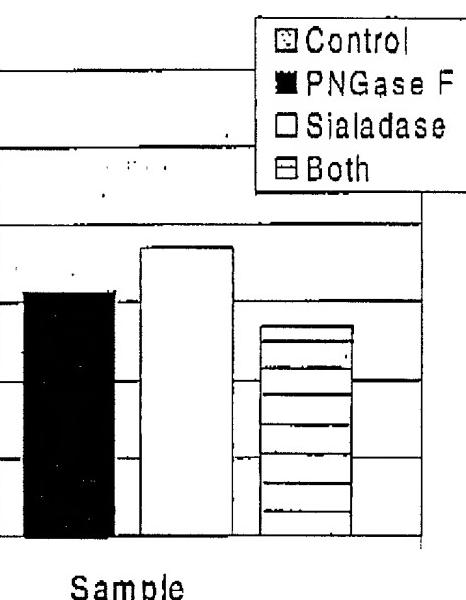
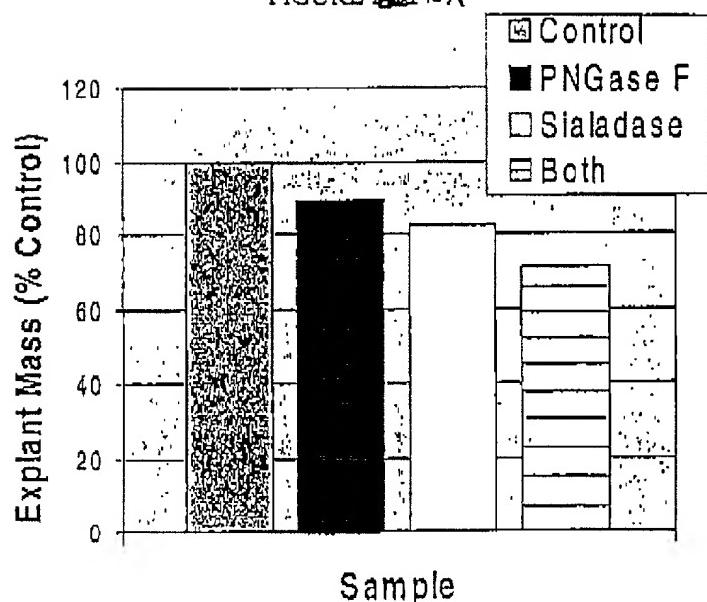


FIGURE 13B

Figure 14 Antibody Listing

Specificity	Antigen	Host Species	PC/MC	Source	Catalog No.
IGF- <b>b1</b> (human)	Protein	Rabbit	Polyclonal	Promega	G1221
IGF- <b>b2</b> (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-90
IGF- <b>b3</b> (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-82
BMP-2 (human)	Protein	Rabbit	Polyclonal	Austral Biologics	PA-513-9
BMP-3 (human)	Peptide	Chicken	Polyclonal	Research Genetics	NA
BMP-4 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-6896
BMP-5 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-7405
BMP-6 (human)	Peptide	Mouse	Monoclonal	Novocastra Laboratories	NCL-BMP6
BMP-7 (mouse)	Peptide	Rabbit	Polyclonal	Research Genetics	NA
FGF-1 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-1884
osteonectin (bovine)	Protein	Mouse	Monoclonal	DSHB	AON-1
osteopalcin (bovine)	Protein	Rabbit	Polyclonal	Accurate Chemicals	A761/R11
serum albumin (bovine)	Protein	Rabbit	Polyclonal	Chemicon International	AB870
transferin (human)	Protein	Chicken	Polyclonal	Chemicon International	AB797
apo-A1 (ipoprotein (human))	Protein	Goat	Polyclonal	Chemicon International	AB740

Figure 15A Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	Best Database Match	Match Identification	Species	Acc. No.	445
1							
2	Ix 49 (1579)	XLAAGAYDVEK	11/11	histone H1.C	human	67668 (NCBI)	165-75
3	Ix 67 (1346)	SLEKVCADLR	11/11	40s Ribosomal Protein S20	rat	R3RT2D (PIR)	31-41
4	Ix 65 0	(Y)VCGMLGFPSEAPV	WVCGMLGFPGEKRV	11/14 LORP	mouse	AAAC95338 (NCBI)	1213-228
5	N terminal seq	STGVLLPLQNNELPG	STGVLLPLQNNELPG	15/15 BMP-3	human	4557371 (NCBI)	290-304
Ix 72 (3923)	STGVLLPLQNNELPGA EYQY	STGVLLPLQNNELPG AEYQY	20/20	BMP-3	human	4557371 (NCBI)	290-309
Ix 74 (3409)	STGVLLPLIQ	STGVLLPLIQ	9/9	BMP-3	human	4557371 (NCBI)	290-298
6	Ix 55 (1586)	(S)QTQLQFQE	SQTQLQFDE	7/8 BMP-3	human	4557371 (NCBI)	346-353
Ix 47	VYAF	no match	7/7				
N terminal seq	IAGCKYSREKKNTTPAP	IAGCKYSREKKNTTPAP	11/14	G2-Macroglobulin Receptor Assoc. Pro.	human	P30533 (Swiss-Prot)	31-45
Ix 57 (1438)	SQTQLQFDEQ	SQTQLQFDEQ	9/9	BMP-3	human	4557371 (NCBI)	346-354
Ix 57 (1852)	SLKPSNHA	SLKPSNHA	8/8	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	410-417
Ix 51 (1093)	AALRPLVKP	AALRPLVKP	9/9	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	418-426
Ix 37 (no MS)	A(H)(Q)VERYV	A(H)(Q)VERYV	5/5	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	108-113
Ix 37 (no MS)	A(H)(Q)VERYV	HQSDRYW	5/7	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	22-29
Ix 78 0	XALFGAQLGALGP	no match	7/7				
Ix 58 (1587)	SQTQLQFDEQT	SQTQLQFDEQT	10/10	BMP-3	human	P12645 (Swiss-Prot)	346-355

Figure 15B Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	Best Database Match	Match	Identification	Species	Acc. No.	AAs
11	fx 55 (131)	SQNLXF	ISQTLQF	5/6	BMP-3	Human	4557371 (NCBI)	348- 351
fx 47 (177)	VLATVTKPVGGDK	VLAIVTKPVGGDK	13/13	60S Ribosomal Protein L6	Human	Q02878 (Swiss-Prot)	87-99	
fx 76 (178)	xFAL	xFAL	4/4	60S Ribosomal Protein L6	Human	Q02878 (Swiss-Prot)	273- 276	
fx 61 (1145)	AVPQLQGYLR	AVPQLQGYLR	9/10	60S Ribosomal Protein L6	Human	Q02878 (Swiss-Prot)	262- 271	
18								
22	fx 58 (101)	ALDAAYCFR	ALDAAYCFR	9/9	TGF-β2	Human	P08112 (Swiss-Prot)	303- 311
fx 69 (no match)	GYMANFCAGACPYL	GYMANFCAGACPYL	14/14	TGF-β2	Human	P08112 (Swiss-Prot)	340- 353	
fx 66 (1411.71)	WNSQSLSPY	WNSQSLSPY	9/9	SPP24	bovine	Q27367 (Swiss-Prot)	42-50	
25	fx 39 (1410)	KAAKPSVP	KAAKPSVP	8/8	Histone H1.x	Human	JCA4226 (PIR)	199- 206
29								

fx = fraction number (molecular weight of fragment, as measured by SDS-PAGE)

Figure 1A Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Diff. Difference	AAS	% Cover-age	Comments
1	4 peaks match with histone H1.c	human	87668 (NCBI)	1172.97	1172.37	0.60	110-121	22	15 MS peaks match with Band 2
				1579.87	1579.71	0.16	55-79		
				1708.47	1707.89	0.58	64-78		
				2011.58	2012.32	-0.74	35-54		
2	3 peaks match with histone H1.c	human	87668 (NCBI)	1579.76	1579.71	0.05	65-79*	16	Identification of selected peptide confirmed by sequence analysis
				1708.02	1707.89	0.13	64-79		
				2012.12	2012.32	-0.20	35-54		
3	7 peaks match with ribosome S20	rat	R3R120 (PIR)	1129.76	1129.40	0.36	50-59	62	15 MS peaks match with Band 1
				1156.21	1156.30	-0.09	76-83		
				1334.46	1334.62	-0.16	58-66		
				1352.13	1351.58	0.55	88-89		
				1518.24	1517.77	0.27	9-21		
				1919.02	1919.19	-0.17	5-21		
				3404.02	3404.87	-0.85	88-119		
4	3 peaks match with Lysyl Oxidase RP	human	NP002309 (Swiss-Pro)	1997.95	1988.27	-0.32	150-167	8	12 MS peaks match with Band 8
				2410.35	2410.63	-0.28	649-669		
				2610.57	2610.10	0.47	455-476		

Figure 16B Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAs	% Coverage	Comments
5	9 peaks match with BMP-3	human	4557371 (NCBI)	1113.32	1113.31	0.01	361-365	48	% coverage calculation is relative to the mature BMP-3. 183 AAs (290-472)
				1438.53	1438.58	-0.05	346-357		
				1566.76	1566.76	0.00	345-357		
				1651.86	1651.91	-0.05	410-424		
				1794.09	1794.02	0.07	346-350		
				2258.46	2266.63	-0.17	374-392		
				2424.45	2424.81	-0.36	373-392		
									Identification of stained peptide confirmed by sequence analysis
				3403.15	3407.77	1.38	262-318		
6	3 peaks match with $\alpha 2$ -Macroglobulin RAP	human	P30533 (Swiss-Pro)	10102.24	10102.15	0.09	283-290	17	
				2382.58	2362.43	0.15	129-150		
				3048.51	3048.52	-0.01	257-282		
	2 peaks match with BMP-3	human	4557371 (NCBI)	1566.93	1566.75	0.18	346-357	15	% coverage calculation is relative to the mature BMP-3. 183 AAs (290-472)
				1651.88	1651.91	-0.03	410-424		

Figure 16C Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Diff-Difference	AAs	% Cover-age	Comments
7	4 peaks match with ribosome L32	mouse	P17932 (Swiss-Pro)	1033.25	1033.17	0.08	67-75	33	
				1093.31	1093.40	-0.09	1-10*		
				1134.72	1134.28	0.44	65-74		
				1449.78	1449.68	0.12	19-29		
	5 peaks match with BMP-3	human	4557371 (NCBI)	1060.42	1060.20	0.22	102-111	21	% coverage calculation is relative to the mature BMP-3, 183 AAS (280-472)
				1113.39	1113.31	0.08	361-363		
				1360.26	1360.58	-0.32	180-200		
				1652.28	1651.91	0.37	410-424		
				1793.62	1794.02	-0.40	346-360		
B	1 peak matches with Lysyl Oxidase RP	human	NP002309 (Swiss-Pro)	2410.37	2410.63	-0.26	645-669	3	12 MS Peaks match with Band 4
9	6 peaks match with BMP-3	human	4557371 (NCBI)	1113.14	1113.31	-0.17	361-363	36	% coverage calculation is relative to the mature BMP-3, 183 AAS (280-472)
				1438.60	1438.58	0.02	346-357		
				1586.77	1566.76	0.01	345-357		
				1651.91	1651.61	0.30	410-424		
				2901.67	2901.19	0.48	41-66		
				3400.94	3407.77	1.17	290-318		

**Figure 1C** Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAs	% Coverage	Comments
11	5 peaks match with BMP-3	human	4557371 (NCBI)	1113.23	1113.31	-0.08	361-383	48	% coverage calculation is relative to the mature BMP-3, 1B3 AAS (290-472)
				1651.73	1651.91	-0.18	410-474		
				1793.58	1794.02	-0.44	346-390		
				2424.24	2424.81	-0.57	378-392		
				3408.34	3407.77	0.57	290-318		
	5 peaks match with ribosome L6	human	Q02876 (Swiss-Prote)	1140.36	1140.23	0.15	114-122	16	
				1526.88	1526.86	0.02	141-155		
				1059.15	1059.12	0.03	10-23		
				1145.36	1145.35	0.01	262-271		
				1386.74	1386.68	0.06	260-271		
18	4 peaks match with TGF-β2	human	P08112 (Swiss-Prote)	1101.20	1101.26	-0.06	303-311	52	
				1175.26	1175.42	-0.16	400-409		
				2240.37	2240.80	-0.23	312-328		
				2691.70	2691.91	-0.21	340-382		
	5 peaks match with SPP24	bovine	Q27967 (Swiss-Prote)	1410.93	1411.60	-0.67	42-53	30	
				1447.59	1447.65	-0.06	113-124		
				1540.94	1540.60	0.04	86-98		
				1869.10	1869.05	0.05	62-77		
				2268.47	2268.57	-0.10	33-53		

Figure 16E Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAS	% Coverage	Comments
22	5 peaks match with TGF-β2	human	P08112 (Swiss-Pro)	1101.15	1101.26	-0.11	303-311	63	
				1175.13	1175.42	-0.29	400-409		
				2084.16	2084.42	-0.26	312-347		
				2240.25	2240.60	-0.35	312-328		
				2691.61	2691.91	-0.30	340-362		
	2 peaks match with SPP24	bovine	Q27967 (Swiss-Pro)	1411.23	1411.60	-0.37	42-53	11	
				1447.40	1447.65	-0.25	113-124		
25	5 peaks match with histone H1x	human	JG4926 (PIR)	1200.46	1200.40	0.06	48-57	14	
				1221.71	1222.35	-0.64	107-118		
				1349.85	1350.52	-0.67	107-119		
				1384.57	1384.59	-0.02	48-58		
				1732.23	1732.97	-0.74	43-57		
	5 peaks match with BMP-3	human	4557371 (NCBI)	1060.43	1060.20	0.23	102-111	34	% coverage calculation is relative to the mature BMP-3, 183 AAS (2SD-472)
				1438.83	1438.58	0.25	340-357		
				1566.92	1568.76	0.16	345-357		
				1651.80	1651.91	-0.11	410-424		
				3408.86	3407.77	1.09	290-318		

Figure 1cF Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass DIFFERENCE	AAS	% Coverage	Comments
29	4 peaks match with BMP-3	human	4557371 (NCBI)	1113.22	1113.31	-0.09	381-368	27	% coverage calculation is relative to the mature BMP-3, 163 AAs (280-472)

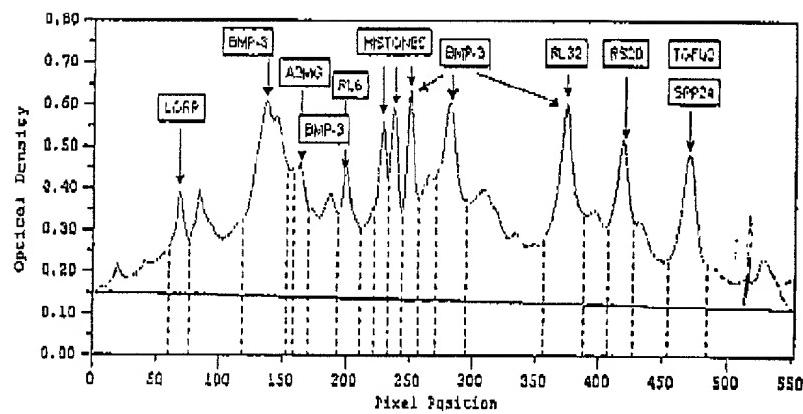


FIGURE 17A



FIGURE 17B

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Figure 18 Quantitation of Identified BP proteins

Identified Protein	Percentage of Total Protein
LORP	2
BMP-3	11
BMP - 3 & A2-MG	3
RL6 & BMP-3	4
Histone	3
Histone	3
Histone & BMP-3	4
BMP-3	8
RL32 & BMP-3	8
RS20	5
SPP24 & TGF- $\beta$ 2	6
Total	58%

Figure 19A Identification of Proteins by Mass Spectrometry of Fragments from 2D Gels

Spot	Digest	Mass Spec Profile	Species	Acc. No.	MS Peaks Data	Database Diff	AAs	% Coverage	Comments
1	Lys-C	2 peaks match with Coagulation Factor XIIIb	Human	P05160 (Swiss-Prot)	1637.01 1921.55 2679.51	1637.44 1921.14 N/A	-0.13 0.51 N/A	472-487 368-382 488-504	
									peptide match confirmed by sequence analysis
2	Trypsin	2 peaks match with LORP	Human	NP002309 (Swiss-Prot)	1609.57	1609.86	-0.31	241-253	5
3	Lys-C	8 peaks match with Cathepsin L Precursor	Bovine	P25075 (Swiss-Prot)	2410.59 1407.26	2410.63 1406.00	0.26 0.46	648-659 105-116	41
					1546.04 1681.16 1681.86 1884.71 2352.90 2381.50 2721.51	1546.70 1660.80 1680.90 1834.00 2351.50 2380.70 2721.10	0.14 0.35 1.06 0.71 1.40 0.80 0.41	58-70 21-33 301-314 318-334 274-285 239-261 131-154	

**Figure 1C** Identification of Proteins by Mass Spectrometry of Fragments from 2D Gels

Figure 7D Identification of Proteins by Mass Spectrometry of Fragments from 2D Gels

Spot	Digest	Mass Spec Profile	Species	Acc. No.	MS Peaks Data	Database Diff	AAS	% Coverage	Comments
9	Trypsin	7 peaks match S38	Mouse	P97351 (Swiss-Proj)	920.05	920.10 -0.05	19-26	29	
					1218.29	1218.31 -0.02	152-161		
					1346.62	1346.49 0.13	151-161		
					1516.69	1516.69 0.00	174-186		
					1593.72	1593.82 -0.10	94-108		
					1719.91	1720.00 -0.09	199-212		
					1953.12	1953.16 -0.04	65-81		
10	Trypsin	4 peaks match H1.c	Human	87668 (NCBI)	1327.75	1327.53 0.19	24-46	23	
					1579.70	1579.71 -0.01	65-79		
					1707.65	1707.89 -0.24	64-79		
					2147.17	2147.53 -0.36	1-21		
11	Trypsin	6 peaks match S4	Human	P12750 (Swiss-Proj)	1168.48	1168.38 0.10	239-239	23	
					1216.39	1216.39 0.00	134-144		
					1354.03	1353.61 0.42	230-241		
					1507.81	1507.88 0.12	198-210		
					1557.75	1557.98 -0.23	37-48		
					2140.34	2140.58 -0.24	221-239		
					2591.80	2591.90 -0.10	77-99		

Figure 20 Quail Chorioallantoic Membrane (CAM) Angiogenesis Assay

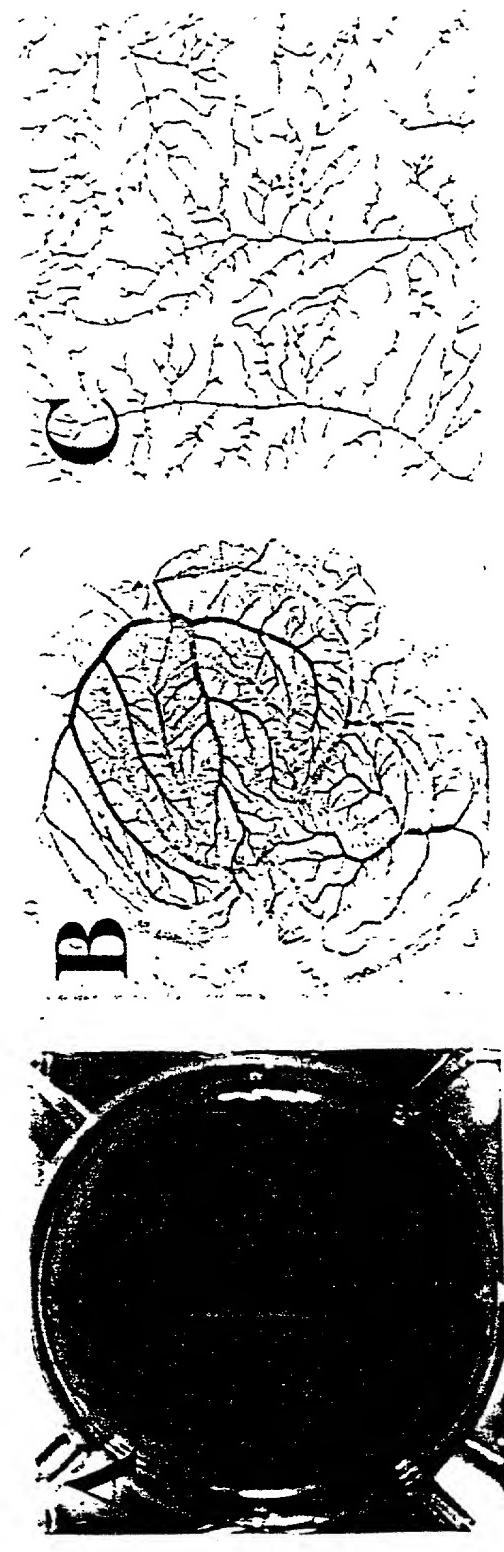


Figure 21 Black and white images of CAM vasculature after growth factor treatment

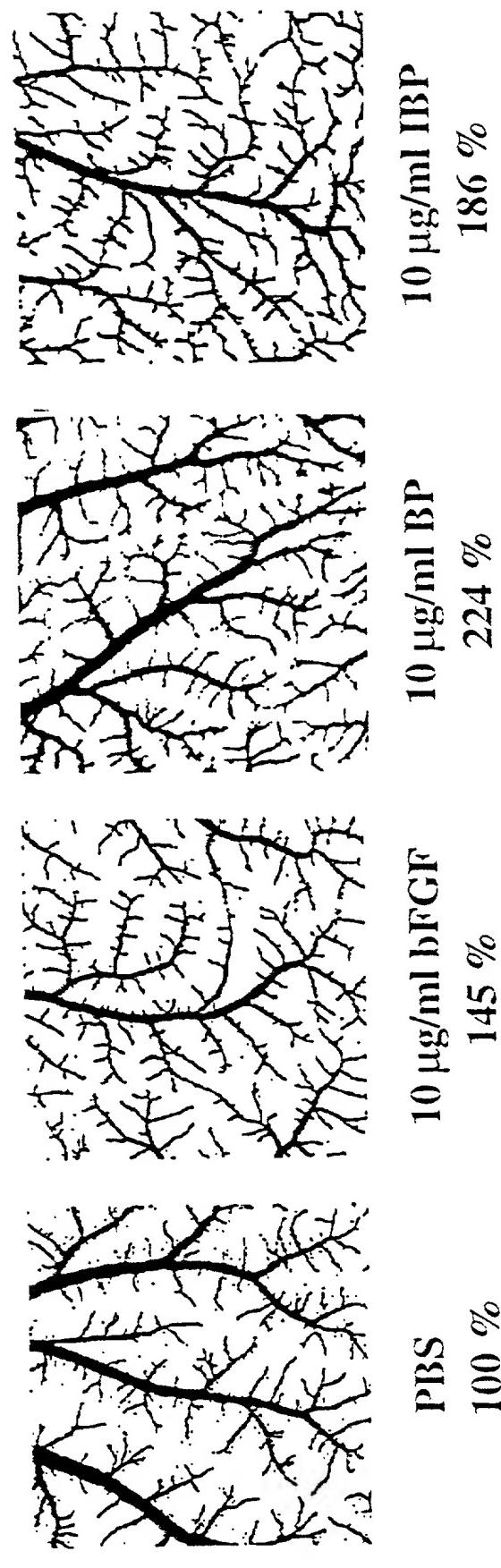
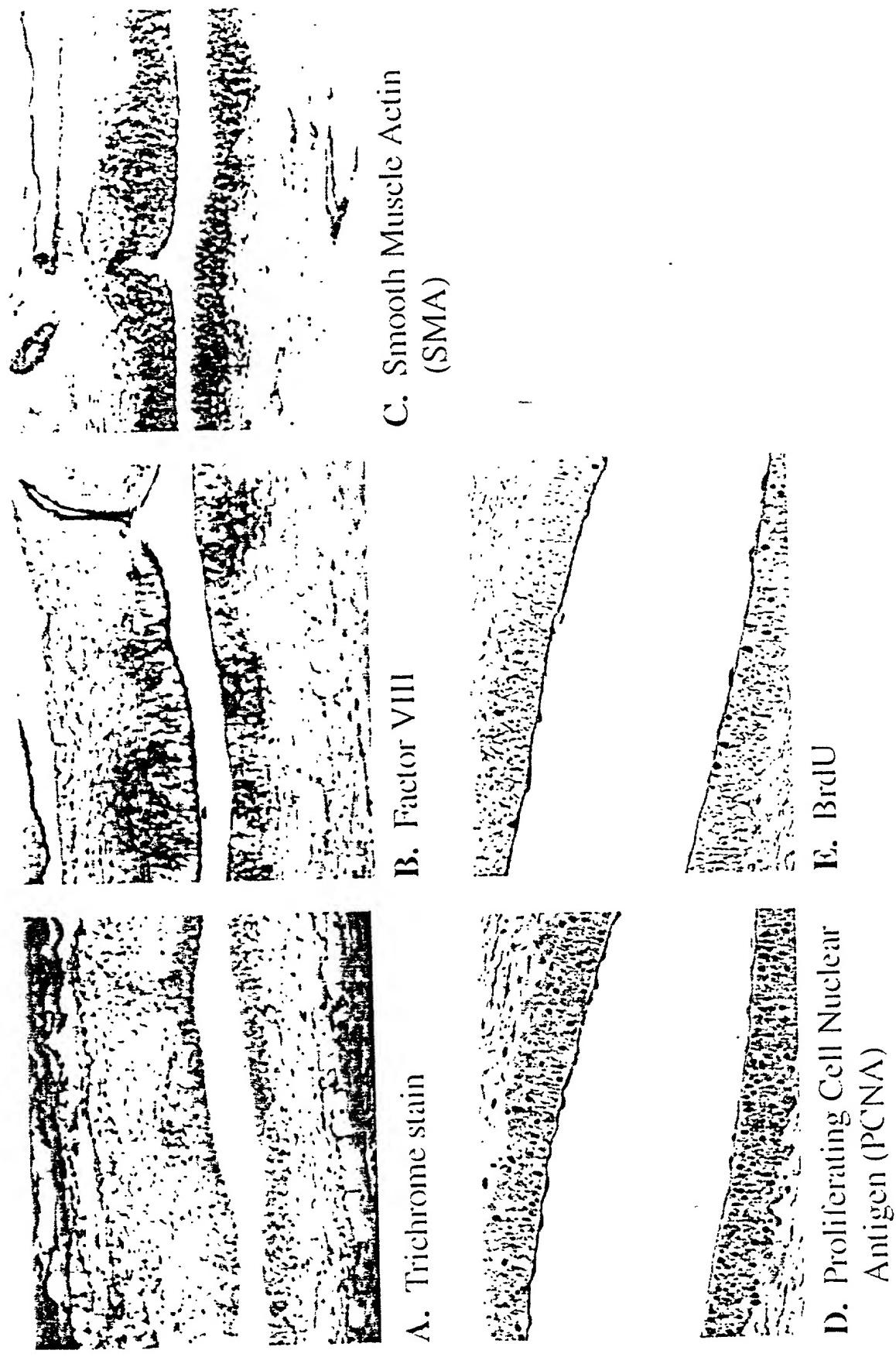


Figure 22 Histological sections of blood vessels formed in canine myocardium 2 weeks following BP injection



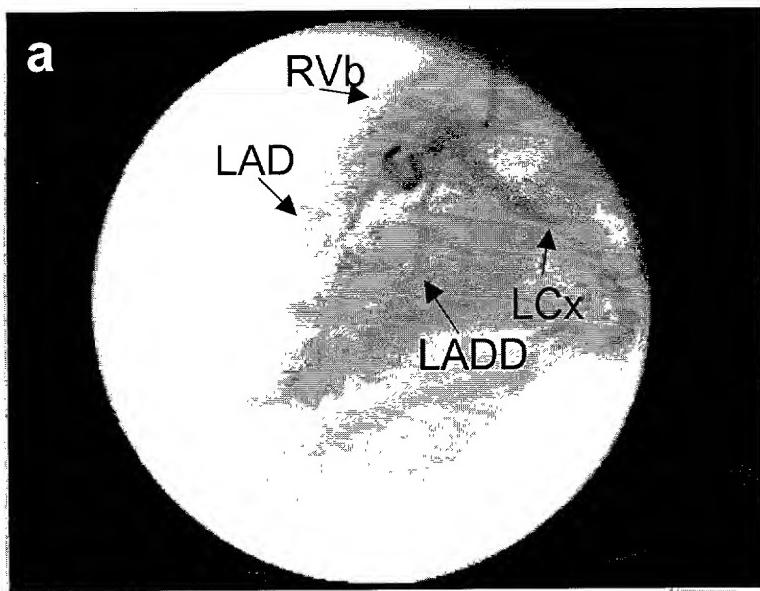


Fig. 23

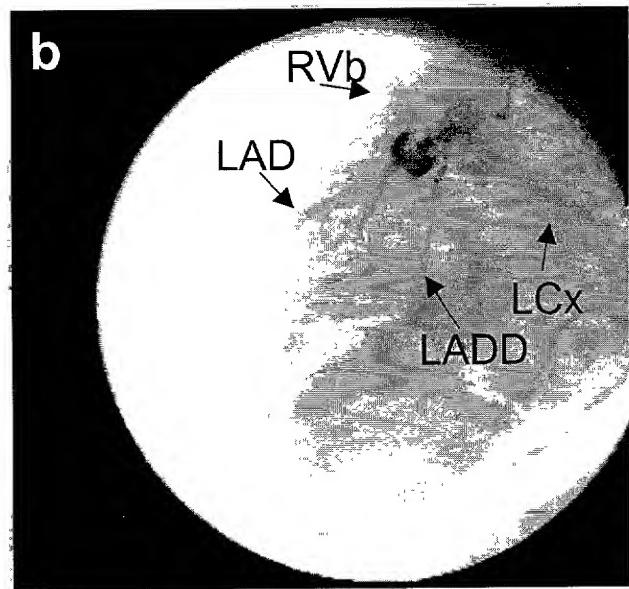


Fig. 24

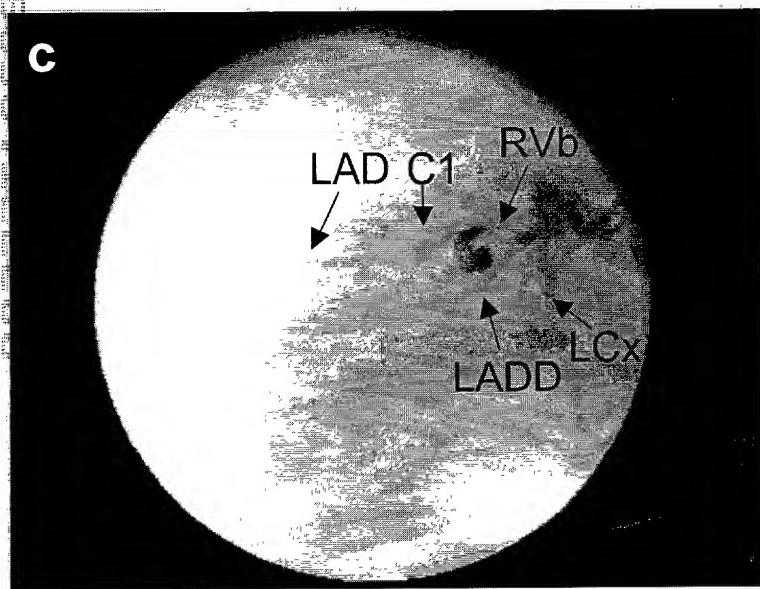


Fig. 25

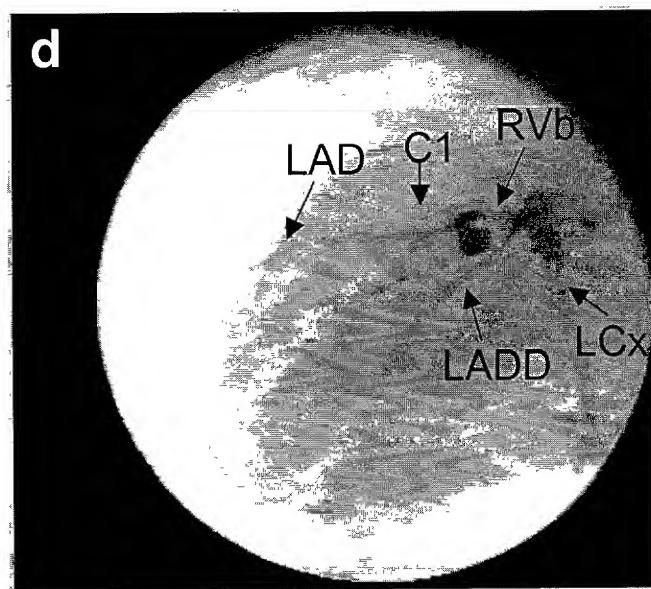


Fig. 26